

ABSTRACT

A protein crystal detection method for detecting protein crystals in a protein solution held in a crystallization vessel. A plurality of cross sections of the protein solution are photographed to form layer images, and each of the layer images is formed into a crystal characteristic image by extracting the characteristic portions of protein crystals. Determining parameters are calculated from layer information which is obtained by digitizing the number of pixels and the number of labels in the characteristic portions. The determining parameters include the number of typical pixels indicating the number of pixels of a layer image having the largest characteristic portion, the number of typical average pixels for each label, and the inter-layer invariability indicating the ratio of the number of pixels in the characteristic portions between two adjacent layers. In crystallization determination, these determining parameters are compared with determining thresholds to distinguish protein crystals from other products by their difference in thickness, thereby determining the growth status of the protein crystals. This provides an apparatus and method for detecting protein crystals with high precision.